#### SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (i) APPLICANT: Dulac, Catherine Axel, Richard
  - (ii) TITLE OF INVENTION: Cloning Of Vertebrate Pheromone Receptors And Uses Thereof
  - (iii) NUMBER OF SEQUENCES: 18
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Cooper & Dunham LLP
    - (B) STREET: 1185 Avenue of the Americas
    - (C) CITY: New York
    - (D) STATE: New York
    - (E) COUNTRY: United States
    - (F) ZIP: 10036
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER:
    - (B) FILING DATE:
    - (C) CLASSIFICATION:
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: White, John P.
    - (B) REGISTRATION NUMBER: 28678
    - (C) REFERENCE/DOCKET NUMBER: 48557
    - (ix) TELECOMMUNICATION INFORMATION:
      - (A) TELEPHONE: 212 278 0400
      - (B) TELEFAX: 212 391 0526

#### (2) INFORMATION FOR SEQ ID NO:1:

(i)	SECUENCE	CHARACTERISTICS:	

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAACATAAGT CCAGTTATCT ACAGGTACAG GTTGATGAGA GGCCTCTCCA TTTCCACCAC 60 CTGCCTGTTG AGTGTCCTCC AGGCCATCAA CCTCACCCCA AGGAGCTCCC GTTTGGCAAT 120 GTTCAGAGAT CCTCACATCA CAAACCGCGT TGCTTTCTCT TGCTGTGGGT CTTCCACATA 180 TCCATTAGTG GAAGCTTCTT AGTCTCCACT CTTCCCTCCA AAAATGTTGC CTCAAATAGT 240 GTTACATTTG TCACTCAATC CTGCTCTGCT GGGCCCCTGA GTTGCTTCCT TGGGCAGACA 300 ATTTTCACAC TGATGACATT TCAGGATGTC TCCTTGCAGC TCATGGCCCC CTTCAGTGGA 360 TACATGGTGA TTCTCTTGTG CAGGCATAAC AGGCAGTCTC AGCATCTTCA TAGTATCAAC 420 CTTTCTCCAA AAGCACCCCC AGATAAAAGG GCCATCCAGA GCATTCTTTT GCTCGTGAGT 480 TTCTTTGTGT TCATGTGCCT TTTCCCATTT GCTGCCTTAA CACTTCTGTC 530

#### (2) INFORMATION FOR SEQ ID NO:2:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: DNA (genomic)

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTCGGCACG	AGTTCACCTG	CCCTCGAATT	TCAATTTGAG	TAAGTGACCA	GCAATGGAGT	60
ACAGAATCAG	AAGATGGTTG	GATCCCAGGC	AGGCTGTGGG	AGGAGGAACT	CTGGAACTGC	120
ATGAGGAGTT	TGAGCACCTG	CCATGGAGTA	GCTGATCTCT	GAGGACCCCT	CACACAGGTC	180
CTGTGTTCTA	CATCAAGTGC	ATATTTTTCC	TAGGATATTC	ATTTCCGTAA	GTCCTGAAAT	240
TACTTAATTT	TTATAGGAGT	TCTCATATAT	GATGAATAAG	AACAGCAGAC	TCTACACTGA	300
TTCTAACATA	AGGAATACCT	TTTTCGCTGA	AATTGGCATT	GGAGTCTCAG	CCAATAGCCT	360
CCTACTTCTC	TTCAACATCT	TCAAGTTAAT	TTGTGGGCAG	AGGTCCAGAC	TCACTGACCT	420
GCCCATTGGT	CTCTTGTCCC	TAATCAACTT	ACTTATGCTA	CTGATGACGG	CATTCATAGC	480
CACAGACACT	TTTATTTCTT	GGAGAGGGTG	GGATGACATC	ATATGTAAAT	CCCTTCTCTA	540
CCTGTACAGA	ACTTTTAGAG	GTCTCTCTCT	TTGTACCAGC	TGCCTGTTGA	GTGTCCTGCA	600
GGCCATCATC	CTCAGTCCCA	GAAGCTCCTG	TTTAGCAAAG	TTCAAACATA	AGCCTTCCCA	660
TCACATCTCC	TGTGCCATTC	TTTCTCTGAG	TGTCCTCTAC	ATGTTCA'ITA	GCAGTCACCT	720
CTTAGTATCC	ATCATTGCCA	CCCCAAATTT	GACCACGAAT	GACTTTATTC	ATGTTACTCA	780
GTGGTGCTCT	ATTCTACCCA	TGAGTTACCT	CATGCAAAGC	ATGTTTTCTA	CACTGCTGGC	840
CATCAGGGAT	GTCTTTCTTA	TTAGTCTCAT	GGTCCTGTCA	ACATGGTACA	TGGTGGCTCT	900
CTTGTGTAGG	CACAGGAAAC	AGACCCGGCA	TCTTCAGGGT	ACCAGCCTTT	CCCCAAAAGC	960
ATCCCCAGAA	CAAAGGGCCA	CCCGTTCCAT	CCTGATGCTC	ATGAGCTTAT	TTGTTCTGAT	1020

GTCTGTCTTT	GACAGCATTG	TCTGCAGCTC	AAGAACTATG	TATCTGAATG	ATCCAATATC	1080
TTATTCTTAT	CAACTATTTA	TGGTGCACAT	CTATGCCACA	GTAAGCCCTT	TTGTGTTTAT	1140
TGTCACTGAA	AAACATATAG	TTAACTCTTT	GAGGTCCATG	TGTGTGAAGG	TGCATGAATG	1200
TTTGAATATT	CCTTGATAGC	AAGCTCCATT	AAGAGGAGCC	AATGTAAGCA	TCAGAACTGT	1260
CAATCATGGC	GTGCTATGTG	CTTTGGCATA	TGTGAAATAT	GAAGTTGTTT	TTCTGTTAAA	1320
ATGATTTACT	TTAACTGACG	AGATGATGAA	CGTAACAGAA	GATTAAACCA	CATCCCCTTT	1380
GATAT						1385

### (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1331 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTGGATCCCC	CGGGCTGCAG	GAATTCGGCA	CGAGCCGTGA	TTAAGGGACT	TTGAACTTTT	60
CAAGGGATTT	GGAGTTTTAT	GAAGAATTTG	AAGATTTACA	GAGTTTACAG	GAATGGAGCT	120
GACCAGCCAC	TATGACATGC	CTTATATCTC	CAAGAGCATA	AATATAAGGC	ATGGCATGAG	180
AGGACCAGCA	GCCACTGTTC	TCATATATGA	TGAATAAGAA	CAGCAGAGTC	CACACTGATT	240
CTACCATAAG	GAATACCTTC	TCCACTGAAA	TTGGCATTGG	AATCTTAGCC	AACAGTTTCC	300
TACTTCTCTT	CCACATCTTC	AAGTTTATTC	GTGGACAGAG	GTCCAGACTC	ACTGACCTGC	360

CCATTGGTC	T CTTGTCCCT	A ATCCACCTA	C TGATGCTAC	T GATGGGGGC.	A TTCATAGCCA	420
TAGACATTT	T TATTTCTTGO	G AGGGGATGG	G ATGACATCA	T ATGTAAATT	C CTTGTCTACT	480
TGTACAGAA	G TTTTAGAGGT	CTCTCTCTT	GTACCACCTO	G CATGTTGAG	I GTCCTGCAGG	540
CCATCACCC'	r cagccccaga	AGCTCCTGTT	TAGCAAAGTT	CAAACATAA	TCTCCCCATC	600
ACGTCTCCT	G TGCCATTATT	' TCGCTGAGCA	TCCTCTACAT	GTTCATTAGO	CAGTCACCTCT	660
TAGTATCCA	r caatgccacc	CCCAATTTGA	CCACGAACAA	CTTTATGCA	GTTACTCAGT	720
CCTGCTACAT	TATACCCTTG	AGTTACCTCA	TGCAAAGCAT	GTTTTCTACA	CTTCTGGCCA	780
TCAGAGATAI	CTCTCTTATT	AGTCTCATGG	TCCTCTCGAC	TTGTTACATG	GAGGTTCTCT	840
TGTGTAGGCA	CAGGAATCAG	ATCCAGCATC	TTCAAGGGAC	CAACCTTTCC	CCAAAAGCAT	900
CTCCAGAACA	AAGGGCCACA	CAGACCATCC	TGATGCTCAT	GACCTTCTTT	GTCCTAATGT	960
CCATTTTCGA	CAGCATTGTC	TCCTGTTCAA	GAACTATGTA	TCTGAATGAT	CCAACATCTT	1020
ACTATATTCA	AATATTTGTA	GTGGACATCT	ATGCCACAGT	CAGCCCTTTT	GTGTTTATGA	1080
GCACTGGAAA	ACATATAGTT	AACTTTTTGA	AGTCCATGTG	TGTGAGGGTG	AAGAATGTTT	1140
GAATATTCAT	TAATGGACAA	GATCCTTTAA	GAGGAGCCAA	TGTAGTCATC	AGAACTGTCA	1200
GTCATGGTGT	GCTGTCTATG	TGCTTTGGTA	AATGTGAATÇ	ATGAAGTTGT	TTTTCTGGTA	1260
AAATGATTTA	CTTTAACCAA	CTCATGATTG	TAAACATGTA	ACAGGAGATT	AAACAATATC	1320
CCCTTCGGAA	A					1331

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTCGGCA	C GAGCAAAGG	CAGGGAAGAT	G CTCCACTGGG	ATGTCATGTC	CTCTATGCTCC	60
ACAGTGGAA	A AGTTGTCACA	A TTGTACAAA	C ACTAAAATTA	CGAATTGCTC	C ACAGGCACTA	120
AAAGCTTCCT	r TAATCCTGTG	CAGGATCTCC	TCAGGTACAG	AGTCCTCCTG	; ATACGTCTAT	180
CTGGTCAGAG	GAAAGAGCTG	ATCAGTCATI	AACAGAGCTG	ATTTGGTCCC	TCCAAGGTCA	240
CATGACAAGG	G ACTGTATGAG	AAAACCAGCA	GTGACATGTC	TATAGAGATC	ATTCTGTGCC	300
ACACCCAGCT	CCATGTTTGG	TTTGTGGTAT	TTGCTTCCTA	TCCACATACA	ATGAATAAAG	360
ACAACACACT	CCATGTTGAC	ACAATCATGA	AAATCACTAT	GTTCTCTGAA	GTGAGTGTTG	420
GCATCTTAGC	TAACAGTATC	CTGTTTTTTG	GTCACCTGTG	CATGCTCCTT	GGAGAGAACA	480
AGCCTAAGCC	CATTCATCTC	TACATTGCAT	CCTTGTCCCT	AACACAACTA	ATGCTGCTTA	540
TAACTATGGG	ACTCATAGCT	GCTGACATGT	TTATTTCTCA	GGGGATATGG	GATTCTACCT	600
CATGCCAGTC	ССТТАТСТАТ	TTGCACAGGC	TTTCGAGGGG	TTTTACCCTT	AGTGCTGCCT	660
GTCTGCTGAA	TGTCTTTTGG	ATGATCACTC	TCAGTTCTAA	AAAATCCTGT	TTAACAAAGT	720
TTAAACATAA	CTCTCCCCAT	CACATCTCAG	GTGCCTTTCT	TCTCCTCTGT	GTTCTCTACA	780
TGTGTTTTAG	CAGTCACCTT	ATTTTATCGA	TTATTGCTAC	CCCTAACTTG	ACCTCAGATA	840
ATTTTATGTA	TGTTACTAAG	TCCTGTTCAT	TTCTACCCAT	GTGTTACTCC	AGAACAAGCA	900
TGTTTTCCAC	AACAATTGCT	GTCAGGGAAG	CCTTTTTTAT	CGGTCTCATG	GCCCTGTCCA	960
GTGGGTACCT	GGTGGCTTTC	CTCTGGAGAC	ACAGGAAGCA	GGCCCAGCAT	CTTCACAGCA	1020

CCGGCCTTTC TTCAAAGTCA TCTCCAGAGC AAAGGGCCAC CGAGACCATC CTGCTGCTTA 1080 TGAGTTTCTT TGTGGTTCTC TACATTTTGG AAAATGTTGT CTTCTACTCA AGGATGAAGT 1140 TCAAGGATGG GTCAACATTC TACTGTGTCC AAATTATTGT GTCCCATAGC TATGCCACTG 1200 TCAGCTCTTT TGTGTTTATT TTCACTGAAA AGCGTATGAC TAAGATATTG AGGTCAGTGT 1260 GTGCCAGAAT AATAAATAAT TGATTATTCA GTGATGGGTA TTGCCCCTTA GAATAAACCA 1320 TTACGTTGTC ATCAGAGGTT TGGGTCATGA CATAATTGGG ACATTCTCTG TCTTAAATTG 1380 ATAAATGAAA TTTTCTTTTT TCCTGTTAAA ACTGTTTCCT TTGTGTGTGG ATGCCCAATA 1440 TATGAAAGAA AACTAAACAC CATGTCCTCT TACATATCCA ACCAAAAAA AAAAAA 1496 (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1053 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTCCCA	CCTCTTCATG	CTCTTTGAAA	AGAACAGATC	TAAGCCCATT	GATCTCTACA	60
TTGCTTTCTT	ATCCTTAACC	CAACTAATGC	TGCTTATAAC	TATTGGACTT	ATAGCTGCAG	120
ACATGTTTAT	GTCTCGGGGG	AGATGGGATT	CTACCACATG	CCAGTCCCTT	ATCTATTTGG	180
ACAGGCTTTT	GAGGGGTTTT	ACCCTTTGTG	CTACCTGTCT	GCTGAATGTC	CTTTGGACCA	240
TCACTCTCAG	TCCTAGAAGC	TCCTGTTTAA	CAACATTTAA	ACATAAATCT	CCCCATCACA	300

rctcaggtgc	CTTTCTTTTC	TTCTGTGTTC	TCTATATATC	TTTTGGCAGT	CACCTCTTTT	360
FATCAACAAT	TGCTACCCCC	AATTTGACTT	CAGATAATTT	TATGTATGTT	ACTAAATCCT	420
GTTCATTTCT	ACCCATGAGT	TACTCCAGAA	CAAGCATGTT	TTCCACACCA	ATGGCCATCA	480
GGAAGCCCT	TCTTATTGGT	CTCATTGGCC	TGTCCAGTGG	GTACATGGTT	GCTTTCCTAT	540
GGAGACACAA	GAATCAGGCC	CGGCATCTTC	ACAGCACCAG	CCTTTCTTCA	AAAGTGTCCC	600
CAGAGCAAAG	GGCCACCAGG	ACCATCATGA	TTCTCATGAG	CTTCTTTGTG	GTTCTCTACA	660
TTTTGGAAAA	TGTTGTCTTC	TACTCTAGGA	TGACATTCAA	GGATGGGTCA	ATGTTCTACT	720
GTGTCCAAAT	TATTGTGTCC	CATAGCTATG	CCACCATCAG	CCCTTTTGTG	TTTATTTGCA	780
CAGAAAAGCG	AAATTAATAT	CTTTGGGGGT	CAATGTCTAG	CAGAATAGTA	AGTATTTGAT	840
TACTCAGTGA	TGGATATGGT	CCCTTAATAT	AAACCAATAT	GTTGTCATAA	TAACTATGGA	900
TCATGACATA	TTGGGGACAT	TCTGTGTCTT	AATTTAAA	TTTTAAAAAA	CTTTTTTTGT	960
GTTTAATCTG	TTTCCCTTGT	GTGTGGATGA	TAAGTATATA	AAGGGAAATT	AAACAGCGTG	1020
TCCCCTCAGA	TATCCAAAAA	АААААААА	AAA			1053

# (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3076 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGCTGCAGG	AATTCGGCAC	GAGTCAGAGT	CCTTCCCTGC	TATGTGTAT	C TGGAGCCAGC	60
GACTCTTCTA	TGGAGAGCAG	CTGTGCAGGC	AGGTGGTGGA	GCGGAAGAAG	GCGTGCTGCT	120
GTGACATCAT	CAAGATGCTG	CCTAGCCCTG	GTCGCTGCT	' CTTCTGAGGA	AGCAGGAGAC	180
TGACCCCTGT	GACAATGACT	TGATGAGTCA	CTCTGTTGTC	TACTTACCCI	' AGTTCTTTGT	240
CCCATACAAT	GAGGAGAATC	AGCACACTGT	ATGGAGTTGT	TGACAAGCAA	GCTATATTTT	300
TCTCTGAAGT	AGTCATCGGG	ATCTCATTCA	ACAGTATCCT	CTTCCTCTTC	CACATCTTTC	360
AGTTCCTTCT	TGAGCGTAGG	CTCCGGATCA	CTGACCTGAT	CATCAGTCTC	TTGGCCCTCA	420
TCCACCTTGG	GATGCTAACA	GTCATGGGAT	TCAGAGCTGT	TGATATTTT	GCATCTCAGA	480
ATGTGTGGAA	TGACATCAAA	TGCAAATCCC	TTGCCCACTT	ACACAGACTT	TTGAGGGGCC	540
TCTCTCTTTG	TGCTACCTGT	CTGCTGAGTA	TCTTCCAGGC	CATCACCCTT	AGCCCCAGAA	600
GCTCCTGTTT	AGCAAAGTTC	AAATATAAAT	CCACACAGCA	CAGCCTGTGT	TCCCTTCTTG	660
TGCTCTGGGC	CTTCTACATG	TCCTGTGGTA	CTCACTACTC	CTTCACCATC	GTTGCTGACT	720
ACAACTTCTC	TTCACGCAGT	CTCATATTTG	TCACTGAATC	CTGCATTATT	TTACCCATGG	780
ATTACATCAC	CAGGGATTTA	TTTTTCATAT	TGGGGATATT	TCGGGATGTG	TCCTTCATAG	840
GTCTCATGGC	CCTCTCCAGC	GGGTACATGG	TGGCCCTCTT	GTGCAGACAC	AGGAAACAGG	900
CCCAGCATCT	TCACAGGACC	AGCCTTTCTC	CAAAAGCATC	CCCAGAGCAA	AGGGCCACCA	960
GGACCATCCT	GTTGCTCATG	AGCTTCTTTG	TGTTGATGTA	CTGCTTGGAC	TGCACCATAT	1020
CCGCCTCCAG	ACTTATGCAC .	AACGGTGAAC	CAATCCACCA	CAGTATTCAG	ATGATGGTCT	1080
CCAATAGCTA :	IGCCACCCTC .	AGCCCTTTGC	TGTTAATTGT	TACTGAAAAT	CGAATTAGTA	1140
GGTTTTTGAA (	GTCCTTGCTA (	GGAAGGACAG	TAGATGCTTA	AGTATTGAGG	GGAGGCAGGC	1200
CCACTAAAGG A	AGCCAATATG (	CTAGCTACTG	AATAATGAAT	CCTGGCCTAG	TCCTCATGCA	1260

ATTCCTGAACA AATTAATACA TGACTCATGC TTCGTTAAAC CTGCTTCTTT TGAAATGTGT 1320
ATTACCAACA CCTGTAGATA TTTGAGTCAA ATTTCTTCAT GTGTATTTCT TCTCAGTGTC 1380
AGTAGGGGAC ATCTGTGACA CTTTCACAGA TTAGGGTAAC TTGTGCACTT ATCAATAAGC 1440
TAAAGTGTAC AGCACATTTT ACTAAGCCAA TTATCTCAAC AGTTTGTTTT CTACCCAATT 1500
AAATATGTAA ATGTTACCAC CAAAAAAAAA AAAAAAAAA 1538

### (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1264 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTGGGGTAAA	ACGGCTCGAT	GACTTCCACA	TGTTTTGCCA	TGGCAGAATC	TGCTCCATGC	60
GGGACAAGAA	AATCTCTTTT	CTGGTCTGAC	GGGCTTACTG	CTGAATTCAC	TGTCGGCGAA	120
GGTAAGTTGA	TGACTCATGA	TGAACCCTGT	TCTATGGCTC	CAGATGACAA	ACATGATCTC	180
ATATCAGGGA	CTTGTTCGCA	CCTTCCCTAA	CAGTATCCTG	TTTTTTGCCC	ACCTCTGCAT	240
GTTCTTTGAA	GAGAACAGGT	CTAAGCCCAT	TGATCTGTGC	ATTGCTTTCT	TATCCTTAAC	300
CCAACTAATG	CTGCTTGTAA	CTATGGGACT	CATAGCTGCA	GACATGTTTA	TGGCTCAGGG	360
GATATGGGAT	ATTACCACAT	GCAGGTCCCT	TATCTATTTT	CACAGACTTT	TGAGGGGTTT	420
CAACCTTTGT	GCTGCCTGTC	TACTGCATAT	CCTTTGGACC	TTCACTCTCA	GTCCTAGAAG	480

CTCCTGTTT	A ACAAAGTTTA	AACATAAAT	C TCCCCATCA	CATCTCAGGT	G CCTATCTTTT	540
CTTCTGTGT	T CTCTATATGT	CCTTTAGCAC	G TCACCTCTT	GTATTGGTC	TTGCTACCTC	600
CAATTTAAC	C TCAGATCATT	TTATGTATGT	TACTCAGTCC	TGCTCACTTC	TACCCATGAG	660
TTACTCCAGA	A ACAAGCACGT	TTTCCTTACT	GATGGTCACC	AGGGAAGTCT	TTCTTATCAG	720
TCTCATGGCC	CTGTCCAGTG	GGTACATGGT	GACTCTCCTA	TGGAGGCACA	AGAAGCAGGC	780
CCAGCATCTI	CACAGCACCA	GACTTTCTTC	AAAAGCATCC	CCACAGCAAA	GGGCCACCAG	840
GACCATCCTG	CTGCTTATGA	CCTTCTTTGT	GGTTTTCTAC	ATTTTAGGCA	CTGTTATCTT	900
CCACTCAAGG	ACTAAGTTCA	AGGATGGGTC	AATCTTCTAC	TGTGTCCAAA	TTATTGTGTC	960
CCATAGCTAT	GCCACTATCA	GCCCATTTGT	GTTTGTTTT	TCTGAAAAGC	GCATAATCAA	1020
GTTTTTTAGA	TCAATGTGTG	GCAGAATAGT	AAATACTTGA	TTATTCACTG	ATGAGTATGG	1080
GTCATGAATA	TAGTCTAGTA	AATTGTGATC	AGAGTTATGG	CTCATGACAT	ATTAAAAACA	1140
TTCTCTAATT	TAAGTTTAAC	ATATAAAATT	ATCTTATTTC	TCTTAAATGT	GTTTACTTTG	1200
TGTGTATTAA	AAGTATGTAA	AAGATAATTA	ATCCCCAAAT	ACACCTTTTT	ТТСАААТТАА	1260
AAAA						1264

# (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 315 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Met Asn Lys Asn Ser Arg Leu Tyr Thr Asp Ser Asn Ile Arg Asn 1 5 10 15

Thr Phe Phe Ala Glu Ile Gly Ile Gly Val Ser Ala Asn Ser Leu Leu 20 25 30

Leu Leu Phe Asn Ile Phe Lys Leu Ile Cys Gly Gln Arg Ser Arg Leu 35 40 45

Thr Asp Leu Pro Ile Gly Leu Leu Ser Leu Ile Asn Leu Leu Met Leu 50 55 60

Leu Met Thr Ala Phe Ile Ala Thr Asp Thr Phe Ile Ser Trp Arg Gly 65 70 75 80

Trp Asp Asp Ile Ile Cys Lys Ser Leu Leu Tyr Leu Tyr Arg Thr Phe
85 90 95

Arg Gly Leu Ser Leu Cys Thr Ser Cys Leu Leu Ser Val Leu Gln Ala 100 105 110

Ile Ile Leu Ser Pro Arg Ser Ser Cys Leu Ala Lys Phe Lys His Lys
115 120 125

Pro Ser His His Ile Ser Cys Ala Ile Leu Ser Leu Ser Val Leu Tyr 130 135 140

Met Phe Ile Ser Ser His Leu Leu Val Ser Ile Ile Ala Thr Pro Asn 145

Leu Thr Thr Asn Asp Phe Ile His Val Thr Gln Trp Cys Ser Ile Leu 165 170 175

Pro Met Ser Tyr Leu Met Gln Ser Met Phe Ser Thr Leu Leu Ala Ile 180 185 190

Arg Asp Val Phe Leu Ile Ser Leu Met Val Leu Ser Thr Trp Tyr Met 195 200 205

Val Ala Leu Leu Cys Arg His Arg Lys Gln Thr Arg His Leu Gln Gly 210 215 220

Thr Ser Leu Ser Pro Lys Ala Ser Pro Glu Gln Arg Ala Thr Arg Ser 225 230 235 240

Ile Leu Met Leu Met Ser Leu Phe Val Leu Met Ser Val Phe Asp Ser 245 250 255

Ile Val Cys Ser Ser Arg Thr Met Tyr Leu Asn Asp Pro Ile Ser Tyr 260 265 270

Ser Tyr Gln Leu Phe Met Val His Ile Tyr Ala Thr Val Ser Pro Phe 275 280 285

Val Phe Ile Val Thr Glu Lys His Ile Val Asn Ser Leu Arg Ser Met 290 295 300

Cys Val Lys Val His Glu Cys Leu Asn Ile Pro 305 310 315

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 311 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Met Asn Lys Asn Ser Arg Leu His Ile Asp Ser Asn Ile Arg Asn 1 5 5 10 10 15

Thr Phe Phe Thr Glu Ile Gly Ile Gly Val Ser Ala Asn Ser Leu Leu 20 25 30

- Leu Leu Phe Asn Ile Phe Lys Phe Ile His Gly Gln Arg Ser Arg Leu 35 40 45
- Thr Asp Leu Pro Ile Gly Leu Leu Ser Leu Ile Asn Leu Leu Met Leu 50 55 60
- Leu Ile Met Ala Cys Ile Ala Thr Asp Ile Phe Ile Ser Cys Arg Arg 65 70 75 80
- Trp Asp Asp Ile Ile Cys Lys Ser Leu Leu Tyr Leu Tyr Arg Thr Phe
  85 90 95
- Arg Gly Leu Ser Leu Ser Thr Thr Cys Leu Leu Ser Val Leu Gln Ala
- Ile Ile Leu Ser Pro Arg Ser Ser Cys Leu Ala Lys Tyr Lys His Lys
  115 120 125
- Pro Pro His His Ile Phe Cys Ala Met Leu Phe Leu Ser Val Leu Tyr 130 135 140
- Leu Thr Thr Asn Asp Phe Ile His Val Ser Gln Ser Cys Ser Ile Leu 165 170 175
- Pro Met Ser Tyr Leu Met Gln Ser Met Phe Ser Thr Leu Leu Ala Ile 180 185 190
- Arg Asn Val Phe Leu Ile Ser Leu Ile Val Leu Ser Thr Trp Tyr Met 195 200 205
- Val Ala Leu Leu Cys Arg His Arg Lys Gln Thr Arg His Leu Gln Asp 210 215 220
- Thr Ser Leu Ser Arg Lys Ala Ser Pro Glu Gln Arg Ala Thr Arg Ser 225 230 235
- Ile Leu Met Leu Arg Ser Leu Phe Gly Leu Met Ser Ile Phe Asp Ser 245 250 255

Ile Ala Ser Cys Ser Arg Thr Met Tyr Leu Asn Asp Pro Thr Ser Tyr 260 265 270

Ser Ile Gln Leu Leu Val Val His Ile Tyr Ala Thr Val Ser Pro Phe 275 280 285

Val Phe Met Ile Thr Glu Lys His Ile Val Asn Tyr Leu Lys Ser Met 290 295 300

Tyr Val Arg Val Leu Asn Val 305 310

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 311 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Met Asn Lys Asn Ser Arg Val His Thr Asp Ser Thr Ile Arg Asn 1 5 10 15

Thr Phe Ser Thr Glu Ile Gly Ile Gly Ile Leu Ala Asn Ser Phe Leu 20 25 30

Leu Leu Phe His Ile Phe Lys Phe Ile Arg Gly Gln Arg Ser Asp Leu 35 40 45

Thr Asp Leu Pro Ile Gly Leu Leu Ser Leu Ile His Leu Leu Met Leu 50 55 60

Leu Met Gly Ala Phe Ile Ala Ile Asp Ile Phe Ile Ser Trp Arg Gly 65 70 75 80

- Trp Asp Asp Ile Ile Cys Lys Phe Leu Val Tyr Leu Tyr Arg Ser Phe 85 90 95
- Arg Gly Leu Ser Leu Cys Thr Thr Cys Met Leu Ser Val Leu Gln Ala
- Ile Thr Leu Ser Pro Arg Ser Ser Cys Leu Ala Lys Phe Lys His Lys
  115 120 125
- Ser Pro His His Val Ser Cys Ala Ile Ile Ser Leu Ser Ile Leu Tyr 130 135 140
- Leu Thr Thr Asn Asn Phe Met Gln Val Thr Gln Ser Cys Tyr Ile Ile 165 170 175
- Pro Leu Ser Tyr Leu Met Gln Ser Met Phe Ser Thr Leu Leu Ala Ile 180 185 190
- Arg Asp Ile Ser Leu Ile Ser Leu Met Val Leu Ser Thr Cys Tyr Met
  195 200 205
- Glu Val Leu Leu Cys Arg His Arg Asn Gln Ile Gln His Leu Gln Gly 210 215 220
- Thr Asn Leu Ser Pro Lys Ala Ser Pro Glu Gln Arg Ala Thr Gln Thr 225 230 235 240
- Ile Leu Met Leu Met Thr Phe Phe Val Leu Met Ser Ile Phe Asp Ser 245 255
- Ile Val Ser Cys Ser Arg Thr Met Tyr Leu Asn Asp Pro Thr Ser Tyr 260 265 270
- Tyr Ile Gln Ile Phe Gly Val Asp Ile Tyr Ala Thr Val Ser Pro Phe 275 280 285
- Val Phe Met Ser Thr Glu Lys His Ile Val Asn Phe Leu Lys Ser Met 290 295 300

Cys Val Arg Val Lys Asn Val 305 310

- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Lys Asp Asn Thr Leu His Val Asp Thr Ile Met Lys Ile Thr 1 5 10 15

Met Phe Ser Glu Val Ser Val Gly Ile Leu Ala Asn Ser Ile Leu Phe
20 25 30

Phe Gly His Leu Cys Met Leu Leu Gly Glu Asn Lys Pro Lys Pro Ile 35 40 45

His Leu Tyr Ile Ala Ser Leu Ser Leu Thr Gln Leu Met Leu Leu Ile 50 55 60

Thr Met Gly Leu Ile Ala Ala Asp Met Phe Ile Ser Gln Gly Ile Trp 65 70 75 80

Asp Ser Thr Ser Cys Gln Ser Leu Ile Tyr Leu His Arg Leu Ser Arg 85 90 95

Gly Phe Thr Leu Ser Ala Ala Cys Leu Leu Asn Val Phe Trp Met Ile 100 105 110

Thr Leu Ser Ser Lys Lys Ser Cys Leu Thr Lys Phe Lys His Asn Ser

Pro His His Ile Ser Gly Ala Phe Leu Leu Cys Val Leu Tyr Met 130 135 140

Cys Phe Ser Ser His Leu Ile Leu Ser Ile Ile Ala Thr Pro Asn Leu 145 150 155 160

Thr Ser Asp Asn Phe Met Tyr Val Thr Lys Ser Cys Ser Phe Leu Pro 165 170 175

Met Cys Tyr Ser Arg Thr Ser Met Phe Ser Thr Thr Ile Ala Val Arg 180 185 190

Glu Ala Phe Phe Ile Gly Leu Met Ala Leu Ser Ser Gly Tyr Leu Val 195 200 205

Ala Phe Leu Trp Arg His Arg Lys Gln Ala Gln His Leu His Ser Thr 210 215 220

Gly Leu Ser Ser Lys Ser Ser Pro Glu Gln Arg Ala Thr Glu Thr Ile 225 230 235 240

Leu Leu Met Ser Phe Phe Val Val Leu Tyr Ile Leu Glu Asn Val
245 250 255

Val Phe Tyr Ser Ser Arg Met Phe Lys Asp Gly Ser Thr Phe Tyr Cys 260 265 270

Val Gln Ile Ile Val Ser His Ser Tyr Ala Thr Val Ser Ser Phe Val 275 280 285

Phe Ile Phe Thr Glu Lys Arg Met Thr Lys Ile Leu Arg Ser Val Cys 290 295 300

Ala Arg Ile Ile Asn Asn 305 310

- (2) INFORMATION FOR SEQ ID NO:12:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 278 amino acids
    - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
- Phe Ser His Leu Phe Met Leu Phe Glu Lys Asn Arg Ser Lys Pro Ile 1 5 10 15
- Asp Leu Tyr Ile Ala Phe Leu Ser Leu Thr Gln Leu Met Leu Leu Ile 20 25 30
- Thr Ile Gly Leu Ile Ala Ala Asp Met Phe Met Ser Arg Gly Arg Trp 35 40 45
- Asp Ser Thr Thr Cys Gln Ser Leu Ile Tyr Leu Asp Arg Leu Leu Arg 50 55 60
- Gly Phe Thr Leu Cys Ala Thr Cys Leu Leu Asn Val Leu Trp Thr Ile 65 70 75 80
- Thr Leu Ser Pro Arg Ser Ser Cys Leu Thr Thr Phe Lys His Lys Ser 85 90 95
- Pro His His Ile Ser Gly Ala Phe Leu Phe Phe Cys Val Leu Tyr Ile
- Ser Phe Gly Ser His Leu Phe Leu Ser Thr Ile Ala Thr Pro Asn Leu 115
- Thr Ser Asp Asn Phe Met Tyr Val Thr Lys Ser Cys Ser Phe Leu Pro 130 135 140
- Glu Ala Leu Leu Ile Gly Leu Ile Gly Leu Ser Ser Gly Tyr Met Val

175

Ala Phe Leu Trp Arg His Lys Asn Gln Ala Arg His Leu His Ser Thr 180 185 190

Ser Leu Ser Ser Lys Val Ser Pro Glu Gln Arg Ala Thr Arg Thr Ile 195 200 205

Met Ile Leu Met Ser Phe Phe Val Val Leu Tyr Ile Leu Glu Asn Val 210 215 220

Val Phe Tyr Ser Arg Met Thr Phe Lys Asp Gly Ser Met Phe Tyr Cys 225 230 235 240

Val Gln Ile Ile Val Ser His Ser Tyr Ala Thr Ile Ser Pro Phe Val 245 250 255

Phe Ile Cys Thr Glu Lys Arg Ile Ile Lys Leu Trp Gly Ser Met Ser 260 265 270

Ser Arg Ile Val Ser Ile 275

DSBGB416 D70301

- (2) INFORMATION FOR SEQ ID NO:13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 310 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Arg Ile Ser Thr Leu Tyr Gly Val Val Asp Lys Gln Ala Ile 1 5 10 15

- 83 -

P	he	Phe	Ser	Glu 20	Val	Val	Ile	Gly	Ile 25	Ser	Phe	Asn	Ser	Ile 30	Leu	Phe
L	eu	Phe	His 35	Ile	Phe	Gln	Phe	Leu 40	Leu	Glu	Arg	Arg	Leu 45	Arg	Ile	Thr
A	sp	Leu 50	Ile	Ile	Ser	Leu	Leu 55	Ala	Leu	Ile	His	Leu 60	Gly	Met	Leu	Thr
	al 5	Met	Gly	Phe	Arg	Ala 70	Val	Asp	Ile	Phe	Ala 75	Ser	Gln	Asn	Val	Trp
A	.sn	Asp	Ile	Lys	Cys 85	Lys	Ser	Leu	Ala	His 90	Leu	His	Arg	Leu	Leu 95	Arg
G	ly	Leu	Ser	Leu 100	Cys	Ala	Thr	Cys	Leu 105	Leu	Ser	Ile	Phe	Gln 110	Ala	Ile
T	hr	Leu	Ser 115	Pro	Arg	Ser	Ser	Cys 120	Leu	Ala	Lys	Phe	Lys 125	Tyr	Lys	Ser
T	hr	Gln 130	His	Ser	Leu	Cys	Ser 135	Leu	Leu	Val	Leu	Trp 140	Ala	Phe	Tyr	Met
	er 45	Cys	Gly	Thr	His	Tyr 150	Ser	Phe	Thr	Ile	Val 155	Ala	Asp	Tyr	Asn	Phe 160
S	er	Ser	Arg	Ser	Leu 165	Ile	Phe	Val	Thr	Glu 170	Ser	Cys	Ile	Ile	Leu 175	Pro
M	et	Asp	Tyr	Ile 180	Thr	Arg	His	Leu	Phe 185	Phe	Ile	Leu	Gly	Ile 190	Phe	Arg
A	sp	Val	Ser 195	Phe	Ile	Gly	Leu	Met 200	Ala	Leu	Ser	Ser	Gly 205	Tyr	Met	Val
A.		Leu 210	Leu	Cys	Arg	His	Arg 215	Lys	Gln	Ala	Gln	His 220	Leu	His	Arg	Thr
	er 25	Leu	Ser	Pro	Lys	Ala 230	Ser	Pro	Glu	Gln	Arg 235	Ala	Thr	Arg	Thr	Ile 240

Leu Leu Met Ser Phe Phe Val Leu Met Tyr Cys Leu Asp Cys Thr
245 250 255

Ile Ser Ala Ser Arg Leu Met His Asn Gly Glu Pro Ile His His Ser 260 265 270

Ile Gln Met Met Val Ser Asn Ser Tyr Ala Thr Leu Ser Pro Leu Leu 275 280 285

Leu Ile Val Thr Glu Asn Arg Ile Ser Arg Phe Leu Lys Ser Leu Leu 290 295 300

Gly Arg Thr Val Asp Ala 305 310

- (2) INFORMATION FOR SEQ ID NO:14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 307 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Met Asn Pro Val Leu Trp Leu Gln Met Thr Asn Met Ile Ser Tyr

1 5 10 15

Gln Gly Leu Val Arg Thr Phe Pro Asn Ser Ile Leu Phe Phe Ala His 20 25 30

Leu Cys Met Phe Phe Glu Glu Asn Arg Ser Lys Pro Ile Asp Leu Cys
35 40 45

Ile Ala Phe Leu Ser Leu Thr Gln Leu Met Leu Val Thr Met Gly
50 55 60

- 85 -

Leu Ile Ala Ala Asp Met Phe Met Ala Gln Gly Ile Trp Asp Ile Thr Thr Cys Arg Ser Leu Ile Tyr Phe His Arg Leu Leu Arg Gly Phe Asn Leu Cys Ala Ala Cys Leu Leu His Ile Leu Trp Thr Phe Thr Leu Ser Pro Arg Ser Ser Cys Leu Thr Lys Phe Lys His Lys Ser Pro His His Ile Ser Gly Ala Tyr Leu Phe Phe Cys Val Leu Tyr Met Ser Phe Ser Ser His Leu Phe Val Leu Val Ile Ala Thr Ser Asn Leu Thr Ser Asp His Phe Met Tyr Val Thr Gln Ser Cys Ser Leu Leu Pro Met Ser Tyr Ser Arg Thr Ser Thr Phe Ser Leu Leu Met Val Thr Arg Glu Val Phe Leu Ile Ser Leu Met Ala Leu Ser Ser Gly Tyr Met Val Thr Leu Leu Trp Arg His Lys Lys Gln Ala Gln His Leu His Ser Thr Arg Leu Ser Ser Lys Ala Ser Pro Gln Gln Arg Ala Thr Arg Thr Ile Leu Leu Leu Met Thr Phe Phe Val Val Phe Tyr Ile Leu Gly Thr Val Ile Phe His Ser Arg Thr Lys Phe Lys Asp Gly Ser Ile Phe Tyr Cys Val Gln Ile 

Ile Val Ser His Ser Tyr Ala Thr Ile Ser Pro Phe Val Phe Val Phe

Ser Glu Lys Arg Ile Ile Lys Phe Phe Arg Ser Met Cys Gly Arg Ile 290 295 300

Val Asn Thr

- (2) INFORMATION FOR SEQ ID NO:15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 173 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
  - Asn Ile Ser Pro Val Ile Tyr Arg Tyr Arg Leu Met Arg Gly Leu Ser

    1 10 15
  - Ile Ser Thr Thr Cys Leu Leu Ser Val Leu Gln Ala Ile Asn Leu Thr
    20 25 30
  - Pro Arg Ser Ser Arg Leu Ala Arg Ser Ser His His Lys Pro Arg Cys
    35 40 45
  - Phe Leu Leu Trp Val Phe His Ile Ser Ile Ser Gly Ser Phe Leu 50 55 60
  - Val Ser Thr Leu Pro Ser Lys Asn Val Ala Ser Asn Ser Val Thr Phe 65 70 75 80
  - Val Thr Gln Ser Cys Ser Ala Gly Pro Leu Ser Cys Phe Leu Gly Gln 85 90 95
  - Thr Ile Phe Thr Leu Met Thr Phe Gln Asp Val Ser Leu Gln Leu Met 100 105 110

Ala Pro Phe Ser Gly Tyr Met Val Ile Leu Leu Cys Arg His Asn Arg

Gln Ser Gln His Leu His Ser Ile Asn Leu Ser Pro Lys Ala Pro Pro 130 135 140

Phe Met Cys Leu Phe Pro Phe Ala Ala Leu Thr Leu Leu 165 170

- (2) INFORMATION FOR SEQ ID NO:16:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 71 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Lys Arg Lys Lys Ser Phe Leu Leu Cys Ile Gly Trp Leu Ala Leu 1 5 10 15

Thr Asp Leu Val Gly Gln Leu Leu Thr Ser Pro Val Val Ile Leu Val 20 25 30

Tyr Leu Ser Gln Arg Arg Trp Glu Gln Leu Asp Pro Ser Gly Arg Leu 35 40 45

Cys Thr Phe Phe Gly Leu Thr Met Thr Val Phe Gly Leu Ser Ser Leu 50 55 60

Leu Val Ala Ser Ala Met Ala 65 70

#### (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly Gln Arg Ser Arg Leu Thr Asp Leu Pro Ile Gly Leu Leu Ser Leu 1 5 10 15

Ile Asn Leu Leu Met Leu Leu Ile Met Ala Cys Ile Ala Thr Asp Ile
20 25 30

Phe Ile Ser Cys Arg Arg Trp Asp Asp Ile Ile Cys Lys Ser Leu Leu 35 40 45

Tyr Leu Tyr Arg Thr Phe Arg Gly Leu Ser Leu Ser Thr Thr Cys Leu 50 55 60

Leu Ser Val Leu Gln Ala Ile Ile Leu Ser 65 70

- (2) INFORMATION FOR SEQ ID NO:18:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 174 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
- Lys Cys Lys Ser Leu Ala His Leu His Arg Leu Leu Arg Gly Leu Ser 1 5 10 15
- Leu Cys Ala Thr Cys Leu Leu Ser Ile Phe Gln Ala Ile Thr Leu Ser 20 25 30
- Pro Arg Ser Ser Cys Leu Ala Lys Ser Thr Gln His Ser Leu Cys Ser 35 40 45
- Leu Leu Val Leu Trp Ala Phe Tyr Met Ser Cys Gly Thr His Tyr Ser 50 55 60
- Phe Thr Ile Val Ala Asp Tyr Asn Phe Ser Ser Arg Ser Leu Ile Phe 65 70 75 80
- Val Thr Glu Ser Cys Ile Ile Leu Pro Met Asp Tyr Ile Thr Arg Asp 85 90 95
- Leu Phe Phe Ile Leu Gly Ile Phe Arg Asp Val Ser Phe Ile Gly Leu 100 105 110
- Met Ala Leu Ser Ser Gly Tyr Met Val Ala Leu Leu Cys Arg His Arg
- Lys Gly Ala Gln His Leu His Arg Thr Ser Leu Ser Pro Lys Ala Ser 130 135 140
- Val Leu Met Tyr Cys Leu Asp Cys Thr Ile Ser Ala Ser Arg 165 170